



1642

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/08/766,350B

DATE: 07/10/2002
 TIME: 11:03:05

Input Set : A:\30414-20003.21.txt
 Output Set: N:\CRF3\07102002\H766350B.raw

SEQUENCE LISTING

- 4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Chatterjee, Malaya
 7 Foon, Kenneth A.
 8 Chatterjee, Sunil K.
 10 (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
 11 11D10 AND METHODS OF USE THEREOF
 13 (iii) NUMBER OF SEQUENCES: 58
 15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: MORRISON & FOERSTER
 17 (B) STREET: 755 PAGE MILL ROAD
 18 (C) CITY: PALO ALTO
 19 (D) STATE: CA
 20 (E) COUNTRY: USA
 21 (F) ZIP: 94304-1018
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/08/766,350B
 C--> 31 (B) FILING DATE: 13-Dec-1996
 32 (C) CLASSIFICATION:
 34 (viii) ATTORNEY/AGENT INFORMATION:
 35 (A) NAME: Polizzi, Catherine M.
 36 (B) REGISTRATION NUMBER: 40,130
 37 (C) REFERENCE/DOCKET NUMBER: 30414-20003.21
 39 (ix) TELECOMMUNICATION INFORMATION:
 40 (A) TELEPHONE: (415) 813-5600
 41 (B) TELEFAX: (415) 494-0792
 42 (C) TELEX: 706141
 45 (2) INFORMATION FOR SEQ ID NO: 1:
 47 (i) SEQUENCE CHARACTERISTICS:
 48 (A) LENGTH: 435 base pairs
 49 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: single
 51 (D) TOPOLOGY: linear
 53 (ii) MOLECULE TYPE: DNA (genomic)
 56 (ix) FEATURE:
 57 (A) NAME/KEY: CDS
 58 (B) LOCATION: 1..435
 60 (ix) FEATURE:

ENTERED

RECEIVED

JUL 16 2002

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/766,350B

DATE: 07/10/2002
TIME: 11:03:05

Input Set : A:\30414-20003.21.txt
Output Set: N:\CRF3\07102002\H766350B.raw

61 (A) NAME/KEY: mat_peptide
 62 (B) LOCATION: 61
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 67 ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 48
 68 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro
 69 -20 -15 -10 -5
 71 GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT 96
 72 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 73 1 5 10
 75 GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 144
 76 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
 77 15 20 25
 79 ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 192
 80 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
 81 30 35 40
 83 AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 240
 84 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
 85 45 50 55 60
 87 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288
 88 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
 89 65 70 75
 91 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336
 92 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
 93 80 85 90
 95 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384
 96 Ser Ser Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
 97 95 100 105
 99 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432
 100 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
 101 110 115 120
 103 GGG 435
 104 Gly
 105 125
 108 (2) INFORMATION FOR SEQ ID NO: 2:
 110 (i) SEQUENCE CHARACTERISTICS:
 111 (A) LENGTH: 145 amino acids
 112 (B) TYPE: amino acid
 113 (D) TOPOLOGY: linear
 115 (ii) MOLECULE TYPE: protein
 117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 119 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro 75
 120 -20 -15 -10 -5
 122 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 123 1 5 10
 125 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
 126 15 20 25
 128 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
 129 30 35 40
 131 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/766,350B

DATE: 07/10/2002
TIME: 11:03:05

Input Set : A:\30414-20003.21.txt
Output Set: N:\CRF3\07102002\H766350B.raw

132 45 50 55 60
134 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
135 65 70 75
137 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
138 80 85 90
140 Ser Ser Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
141 95 100 105
143 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
144 110 115 120
146 Gly
147 125

149 (2) INFORMATION FOR SEQ ID NO: 3:
151 (i) SEQUENCE CHARACTERISTICS:
152 (A) LENGTH: 461 base pairs
153 (B) TYPE: nucleic acid
154 (C) STRANDEDNESS: single
155 (D) TOPOLOGY: linear
157 (ii) MOLECULE TYPE: DNA (genomic)
160 (ix) FEATURE:
161 (A) NAME/KEY: CDS
162 (B) LOCATION: 1..459
164 (ix) FEATURE:
165 (A) NAME/KEY: mat_peptide
166 (B) LOCATION: 58

169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
171 ATG GAA TGC AGC TGG GTC TTT CTC TTC CTG TCA ATA ACT ACA GGT 48
172 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
173 -19 -15 -10 -5
175 GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG 96
176 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
177 1 5 10
179 TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG 144
180 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
181 15 20 25
183 ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG 192
184 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
185 30 35 40 45
187 GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT 240
188 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
189 50 55 60
191 CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC 288
192 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
193 65 70 75
195 ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC 336
196 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
197 80 85 90
199 TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT 384
200 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
201 95 100 105

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/766,350B

DATE: 07/10/2002
TIME: 11:03:05

Input Set : A:\30414-20003.21.txt
Output Set: N:\CRF3\07102002\H766350B.raw

203	CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC	432
204	Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro	
205	110 115 120 125	
207	GTC TAT CCA CTG GTC CCT GGA AGC TTG GG	461
208	Val Tyr Pro Leu Val Pro Gly Ser Leu	
209	130	
212	(2) INFORMATION FOR SEQ ID NO: 4:	
214	(i) SEQUENCE CHARACTERISTICS:	
215	(A) LENGTH: 153 amino acids	
216	(B) TYPE: amino acid	
217	(D) TOPOLOGY: linear	
219	(ii) MOLECULE TYPE: protein	
221	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
223	Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly	
224	-19 -15 -10 -5	
226	Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg	
227	1 5 10	
229	Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu	
230	15 20 25	
232	Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu	
233	30 35 40 45	
235	Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn	
236	50 55 60	
238	Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser	
239	65 70 75	
241	Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val	
242	80 85 90	
244	Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly	
245	95 100 105	
247	Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro	
248	110 115 120 125	
250	Val Tyr Pro Leu Val Pro Gly Ser Leu	
251	130	
253	(2) INFORMATION FOR SEQ ID NO: 5:	
255	(i) SEQUENCE CHARACTERISTICS:	
256	(A) LENGTH: 321 base pairs	
257	(B) TYPE: nucleic acid	
258	(C) STRANDEDNESS: single	
259	(D) TOPOLOGY: linear	
265	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
267	GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
269	CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
271	GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTGCCAAA	180
273	AGGTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
275	GAAGATTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG	300
277	GGGACCAAGC TGGAAATAAA A	321
279	(2) INFORMATION FOR SEQ ID NO: 6:	
281	(i) SEQUENCE CHARACTERISTICS:	
282	(A) LENGTH: 321 base pairs	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/766,350B

DATE: 07/10/2002
TIME: 11:03:05

Input Set : A:\30414-20003.21.txt
Output Set: N:\CRF3\07102002\H766350B.raw

283	(B) TYPE: nucleic acid	
284	(C) STRANDEDNESS: single	
285	(D) TOPOLOGY: linear	
291	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
293	GANATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
295	CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
297	GATGGAACCTT TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCACAAA	180
299	AGGTTCACTG GCAGTAGGTC TGGGTCAAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
301	GAAGATTTTG TAGACTATTAA CTGTCTACAA TATGCTAGTT GTCCGTACAC GTTCGGAGGG	300
303	GGCACCAAGC TGGAAATCAA A	321
305	(2) INFORMATION FOR SEQ ID NO: 7:	
307	(i) SEQUENCE CHARACTERISTICS:	
308	(A) LENGTH: 321 base pairs	
309	(B) TYPE: nucleic acid	
310	(C) STRANDEDNESS: single	
311	(D) TOPOLOGY: linear	
317	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
319	GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
321	CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
323	GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCACAAA	180
325	AGGTTCACTG GCAGTAGGTC TGGGTCAAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
327	GAAGATTTTG TAGACTATTAA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA	300
329	GGCACCAAGC TGGAAATCAA A	321
331	(2) INFORMATION FOR SEQ ID NO: 8:	
333	(i) SEQUENCE CHARACTERISTICS:	
334	(A) LENGTH: 321 base pairs	
335	(B) TYPE: nucleic acid	
336	(C) STRANDEDNESS: single	
337	(D) TOPOLOGY: linear	
343	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
345	GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
347	CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
349	GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCACAAA	180
351	AGGTTCACTG GCAGTAGGTC TGGGTCAAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
353	GAAGATTTTG TAGACTATTAA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA	300
355	GGCACCAAGC TGGAAATCAA A	321
357	(2) INFORMATION FOR SEQ ID NO: 9:	
359	(i) SEQUENCE CHARACTERISTICS:	
360	(A) LENGTH: 321 base pairs	
361	(B) TYPE: nucleic acid	
362	(C) STRANDEDNESS: single	
363	(D) TOPOLOGY: linear	
369	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
371	GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
373	CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
375	GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCACAAA	180
377	AGGTTCACTG GCAGTAGGTC TGGGTCAAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
379	GAAGATTTTG TAGACTATTAA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA	300
381	GGCACCAAGC TGGAAATCAA A	321